

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/561,098
Source: IFWP
Date Processed by STIC: 1/3/06

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IFWP

RAW SEQUENCE LISTING

DATE: 01/03/2006

PATENT APPLICATION: US/10/561,098

TIME: 11:04:01

Input Set : A:\PTO.RJ.txt

Output Set: N:\CRF4\01032006\J561098.raw

5 <110> APPLICANT: DE WILDE, Gert Jules Hector
 6 SAUNDERS, Michael John Scott
 7 LOGGHE, Marc Georges
 11 <120> TITLE OF INVENTION: ALCOHOL DEHYDROGENASE SEQUENCES USEFUL FOR DEVELOPING
 COMPOUNDS FOR THE
 12 PREVENTION AND/OR TREATMENT OF METABOLIC DISEASES
 16 <130> FILE REFERENCE: D0590.70042US01
 C--> 20 <140> CURRENT APPLICATION NUMBER: US/10/561,098
 C--> 20 <141> CURRENT FILING DATE: 2005-12-16
 20 <160> NUMBER OF SEQ ID NOS: 9
 24 <170> SOFTWARE: PatentIn version 3.1
 28 <210> SEQ ID NO: 1
 30 <211> LENGTH: 465
 32 <212> TYPE: PRT
 34 <213> ORGANISM: Caenorhabditis elegans
 38 <400> SEQUENCE: 1
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 41 1 5 10 15
 44 Cys Cys Pro His His Ala Pro Ala Thr Asn Pro Phe Lys Leu Ala Lys
 45 20 25 30
 48 Leu His Gly Asn Asn Lys Ser Thr Asp Tyr Ala Phe Glu Met Val Cys
 49 35 40 45
 52 Ser Thr Leu Arg Phe Gly Lys Gly Val Thr Leu Glu Ile Gly Tyr Asp
 53 50 55 60
 56 Val Arg Asn Leu Gly Ala Lys Lys Thr Leu Leu Ile Thr Asp Lys Asn
 57 65 70 75 80
 60 Val Gln Asn Thr Ile Ala Phe Lys Asn Ala Glu Gln Ala Leu Lys Met
 61 85 90 95
 64 Val Asn Ile Glu Tyr Glu Val Phe Asp Asp Val Leu Ile Glu Pro Thr
 65 100 105 110
 68 Val Asn Ser Met Gln Lys Ala Ile Ala Phe Ala Lys Ser Lys Gln Phe
 69 115 120 125
 72 Asp Ser Phe Ile Ala Val Gly Gly Gly Ser Val Ile Asp Thr Thr Lys
 73 130 135 140
 76 Ala Ala Ala Leu Tyr Ala Ser Asn Pro Glu Ala Asp Phe Leu Asp Phe
 77 145 150 155 160
 80 Val Gly Pro Pro Phe Gly Lys Ser Met Gln Pro Lys Asn Pro Met Leu
 81 165 170 175
 84 Pro Leu Ile Ala Val Pro Thr Thr Ala Gly Thr Gly Ser Glu Thr Thr
 85 180 185 190
 88 Ala Ala Ala Ile Met Asp Leu Pro Glu His Lys Cys Lys Thr Gly Ile
 89 195 200 205
 92 Arg Leu Arg Cys Ile Lys Pro Tyr Leu Ala Val Val Asp Pro Leu Asn
 93 210 215 220

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97 225                230                235                240
100 Leu Cys His Ala Leu Glu Ser Phe Thr Ala Leu Pro Phe Asp Gln Arg
101                245                250                255
104 Ser Pro Arg Pro Glu Asn Pro Gly Val Arg Pro Leu Tyr Gln Gly Ser
105                260                265                270
108 Asn Pro Ile Ser Asp Val Trp Ser Lys Glu Ala Leu Arg Ile Ile Gly
109                275                280                285
112 Lys Tyr Phe Arg Arg Ser Ile Phe Asp Pro Thr Asp Glu Glu Ala Arg
113                290                295                300
116 Thr Glu Met Leu Lys Ala Ser Ser Phe Ala Gly Ile Gly Phe Gly Asn
117 305                310                315                320
120 Ala Gly Val His Leu Cys His Gly Leu Ser Tyr Pro Ile Ser Ser Gln
121                325                330                335
124 Ala Lys Ser Cys Val Ala Asp Asp Tyr Pro Lys Glu Lys Asn Leu Ile
125                340                345                350
128 Pro His Gly Leu Ser Val Met Thr Thr Ala Val Ala Asp Phe Glu Phe
129                355                360                365
132 Thr Thr Ala Ala Cys Pro Asp Arg His Leu Ile Ser Ala Gln Thr Leu
133                370                375                380
136 Gly Ala Asp Ile Pro Asn Asn Ala Ser Asn Glu Tyr Ile Ser Arg Thr
137 385                390                395                400
140 Leu Cys Asp Arg Leu Arg Gly Tyr Met Arg Asp Phe Gly Val Pro Asn
141                405                410                415
144 Gly Leu Lys Gly Met Gly Phe Glu Phe Ser Asp Ile Glu Met Leu Thr
145                420                425                430
148 Glu Ala Ala Ser His Ser Val Pro Asn Ile Ala Ile Ser Pro Lys Ser
149                435                440                445
152 Ala Asp Arg Glu Ile Ile Ser Thr Leu Tyr Glu Lys Ser Leu Thr Val
153                450                455                460
156 Tyr
157 465
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162 <211> LENGTH: 1398
164 <212> TYPE: DNA
166 <213> ORGANISM: Caenorhabditis elegans
170 <400> SEQUENCE: 2
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173 catgccccag ctacaaatcc attcaaactt gcaaagcttc atggaaataa caagtcaaca      120
175 gattacgcgt tcgagatggg gtgctcaact cttcgtttcg gaaaaggagt cacgttggag      180
177 attggatacg acgtccgtaa tctcggagca aagaaaacgt tgcttatcac tgataagaat      240
179 gtgcagaata cgatcgcttt taaaaacgcc gagcaagcct taaaaatggg gaatatcgag      300
181 tatgaggtgt ttgatgatgt gctcattgag ccaaccgtca acagtatgca gaaagcaatc      360
183 gcatttgcca aatcgaagca attcgatagt ttcacgctg ttggtggagg atctgtgatc      420
185 gacacgacga aggctgcagc tctatatgct tctaattccag aagcggactt cctcgacttt      480
187 gttggaccac cattcggaat atccatgcaa ccaaagaacc caatgctccc attgatcgct      540
189 gtgccaacaa ctgctggaac tggatccgag actaccgcgg ctgcaatcat ggatcttcca      600
191 gagcacaagt gcaagactgg aatcagactt cgttgcacat agccgtactt ggcagttgtg      660
193 gatccgttga atgtgatgag tatgcctcga aacgtggcaa tctattctgg tttcgatggt      720

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195 ctctgtcacg cgttggaag cttcacagct ttgccattcg atcaaagatc tccacgccct 780
197 gagaatccag gagttcgtcc actttatcaa ggttccaacc cgatcagtga tgtctggagt 840
199 aaagaggctt tgagaatcat tggaaaatac ttccgccgtt ctatcttcga tccaaccgac 900
201 gaagaagctc gtacagaaat gctcaaggct agttcatttg ctgggattgg attcggaaac 960
203 gctgggggtc atctttgccg cgactctcc tacccaatca gctcccaggc gaaaagctgt 1020
205 gtggctgatg attatccaaa ggagaagaac ttgattccac atggactctc tgtaatgaca 1080
207 accgcagtggt ctgatttcga gtttacaact gccgcgtgcc cagatagaca tttgatttct 1140
209 gcacagactc ttggtgcaga tattccgaac aatgccagca atgagtacat ttcccgaact 1200
211 ctttgtgatc ggctgagagg ttatatgcga gactttggag ttccaaatgg actgaaagga 1260
213 atgggattcg aattttctga tattgaaatg cttactgaag cagccagcca ctccgtccca 1320
215 aatattgcaa tctctccaaa gtctgcggat cgtgaaatta tcagcactct gtacgagaag 1380
217 tcccttacgg tttattag 1398
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222 <211> LENGTH: 23
224 <212> TYPE: DNA
226 <213> ORGANISM: Artificial sequence
230 <220> FEATURE:
232 <223> OTHER INFORMATION: primer
234 <400> SEQUENCE: 3
235 gatgatgtgc tcattgagcc aac 23
238 <210> SEQ ID NO: 4
240 <211> LENGTH: 21
242 <212> TYPE: DNA
244 <213> ORGANISM: Artificial sequence
248 <220> FEATURE:
250 <223> OTHER INFORMATION: primer
252 <400> SEQUENCE: 4
253 atatttggga cggagtggct g 21
256 <210> SEQ ID NO: 5
258 <211> LENGTH: 1163
260 <212> TYPE: DNA
262 <213> ORGANISM: Caenorhabditis elegans
266 <400> SEQUENCE: 5
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269 tcgaagcaat tcgatagttt catcgctggt ggtggaggat ctgtgatcga cagcaggaag 120
271 gctgcagctc tatatgcttc taatccagaa gcggacttcc tcgactttgt tggaccacca 180
273 ttccgaaaaat ccatgcaacc aaagaacca atgctcccat tgatcgctgt gccacaact 240
275 gctggaactg gatccgagac taccgcggct gcaatcatgg atcttcaga gcacaagtgc 300
277 aagactggaa tcagacttcg ttgcatcaag ccgtacttgg cagttgtgga tccgttgaat 360
279 gtgatgagta tgctcgaaa cgtggcaatc tattctgggt tcgatgttct ctgtcacgcg 420
281 ttggaaagct tcacagcttt gccattcgat caaagatctc cagccctga gaatccagga 480
283 gttcgtccac tttatcaagg ttccaaccgg atcagtgatg tctggagtaa agaggctttg 540
285 agagtgaagt ggaatttcaa ccatgaagct ctaaatgaat ttatataatt tcagatcatt 600
287 ggaaaatact tccgccgttc tatcttcgat ccaaccgacg aagaagctcg tacagaaatg 660
289 ctcaaggcta gttcatttgc tgggattgga ttccgaaacg ctggggttca tctttgccac 720
291 ggactctcct acccaatcag ctcccaggcg aaaagctgtg tggctgatga ttatccaaag 780
293 gagaagaact tgattccaca tggactctct gtaatgacaa ccgcagtggc tgatttcgag 840
295 tttacaactg ccgcgtgccc agatagacat ttgatttctg cacagactct tgggtgcagat 900
297 attccggtat gtaaattggc caccaagatg gttctgaact aactagatat ttccagaaca 960

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299 atgccagcaa tgagtacatt tcccgaactc tttgtgatcg gctgagaggt tatatgcgag 1020
301 acttttgaggt tccaaatgga ctgaaaggaa tgggattcga attttctgat attggtagaa 1080
303 cacctctctc tagttgaact gccttatatt atactatatt cagaaatgct tactgaagca 1140
305 gccagccact ccgtcccaaa tat 1163
308 <210> SEQ ID NO: 6
310 <211> LENGTH: 467
312 <212> TYPE: PRT
314 <213> ORGANISM: Homo sapiens
318 <400> SEQUENCE: 6
320 Met Ala Ala Ala Ala Arg Ala Arg Val Ala Tyr Leu Leu Arg Gln Leu
321 1 5 10 15
324 Gln Arg Ala Ala Cys Gln Cys Pro Thr His Ser His Thr Tyr Ser Gln
325 20 25 30
328 Ala Pro Gly Leu Ser Pro Ser Gly Lys Thr Thr Asp Tyr Ala Phe Glu
329 35 40 45
332 Met Ala Val Ser Asn Ile Arg Tyr Gly Ala Ala Val Thr Lys Glu Val
333 50 55 60
336 Gly Met Asp Leu Lys Asn Met Gly Ala Lys Asn Val Cys Leu Met Thr
337 65 70 75 80
340 Asp Lys Asn Leu Ser Lys Leu Pro Pro Val Gln Val Ala Met Asp Ser
341 85 90 95
344 Leu Val Lys Asn Gly Ile Pro Phe Thr Val Tyr Asp Asn Val Arg Val
345 100 105 110
348 Glu Pro Thr Asp Ser Ser Phe Met Glu Ala Ile Glu Phe Ala Gln Lys
349 115 120 125
352 Gly Ala Phe Asp Ala Tyr Val Ala Val Gly Gly Gly Ser Thr Met Asp
353 130 135 140
356 Thr Cys Lys Ala Ala Asn Leu Tyr Ala Ser Ser Pro His Ser Asp Phe
357 145 150 155 160
360 Leu Asp Tyr Val Ser Ala Pro Ile Gly Lys Gly Lys Pro Val Ser Val
361 165 170 175
364 Pro Leu Lys Pro Leu Ile Ala Val Pro Thr Thr Ser Gly Thr Gly Ser
365 180 185 190
368 Glu Thr Thr Gly Val Ala Ile Phe Asp Tyr Glu His Leu Lys Val Lys
369 195 200 205
372 Ile Gly Ile Thr Ser Arg Ala Ile Lys Pro Thr Leu Gly Leu Ile Asp
373 210 215 220
376 Pro Leu His Thr Leu His Met Pro Ala Arg Val Val Ala Asn Ser Gly
377 225 230 235 240
380 Phe Asp Val Leu Cys His Ala Leu Glu Ser Tyr Thr Thr Leu Pro Tyr
381 245 250 255
384 His Leu Arg Ser Pro Cys Pro Ser Asn Pro Ile Thr Arg Pro Ala Tyr
385 260 265 270
388 Gln Gly Ser Asn Pro Ile Ser Asp Ile Trp Ala Ile His Ala Leu Arg
389 275 280 285
392 Ile Val Ala Lys Tyr Leu Lys Arg Ala Val Arg Asn Pro Asp Asp Leu
393 290 295 300
396 Glu Ala Arg Ser His Met His Leu Ala Ser Ala Phe Ala Gly Ile Gly
397 305 310 315 320

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400 Phe Gly Asn Ala Gly Val His Leu Cys His Gly Met Ser Tyr Pro Ile
 401 325 330 335
 404 Ser Gly Leu Val Lys Met Tyr Lys Ala Lys Asp Tyr Asn Val Asp His
 405 340 345 350
 408 Pro Leu Val Pro His Gly Leu Ser Val Val Leu Thr Ser Pro Ala Val
 409 355 360 365
 412 Phe Thr Phe Thr Ala Gln Met Phe Pro Glu Arg His Leu Glu Met Ala
 413 370 375 380
 416 Glu Ile Leu Gly Ala Asp Thr Arg Thr Ala Arg Ile Gln Asp Ala Gly
 417 385 390 395 400
 420 Leu Val Leu Ala Asp Thr Leu Arg Lys Phe Leu Phe Asp Leu Asp Val
 421 405 410 415
 424 Asp Asp Gly Leu Ala Ala Val Gly Tyr Ser Lys Ala Asp Ile Pro Ala
 425 420 425 430
 428 Leu Val Lys Gly Thr Leu Pro Gln Glu Arg Val Thr Lys Leu Ala Pro
 429 435 440 445
 432 Cys Pro Gln Ser Glu Glu Asp Leu Ala Ala Leu Phe Glu Ala Ser Met
 433 450 455 460
 436 Lys Leu Tyr
 437 465

440 <210> SEQ ID NO: 7

442 <211> LENGTH: 1831

444 <212> TYPE: DNA

446 <213> ORGANISM: Homo sapiens

450 <400> SEQUENCE: 7

451	gaagaggact	ccaagcgcca	tggccgctgc	cgccccgagcc	cgggtcgcgt	acttgctgag	60
453	gcaactgcaa	cgcgacgcgt	gccagtggcc	aactcattct	catacttact	cccaagcccc	120
455	tggactttca	ccttctggga	aaacaacaga	ttatgccttt	gagatggctg	tttcaaatat	180
457	tagatatgga	gcagcagtta	caaaggaagt	aggaatggac	ctaaaaaaca	tgggtgctaa	240
459	aaatgtgtgc	ttgatgacag	acaagaacct	ctccaagctc	cctcctgtgc	aagtagctat	300
461	ggattcccta	gtgaagaatg	gcacccctt	tacggtttat	gataatgtga	gagtgggaacc	360
463	aacggattca	agcttcattg	aagctattga	gtttgcccaa	aagggagctt	ttgatgccta	420
465	tgttgctgtc	ggtgggtggc	ctaccattga	cacctgtaag	gctgctaata	tgtatgcata	480
467	cagccctcat	tctgatttcc	tagattatgt	cagtggcccc	attggcaagg	gaaagcctgt	540
469	gtctgtgcct	cttaagcctc	tgattgcagt	gccaactacc	tcaggaaccg	ggagtgaaac	600
471	tactgggggt	gccatttttg	actatgaaca	cttgaaagta	aaaattggta	tcacttcgag	660
473	agccatcaaa	cccacactgg	gactgattga	tcctctgcac	accctccaca	tgctgccccg	720
475	agtggctgcc	aacagtggct	ttgatgtgct	ttgccatgcc	ctggagtcac	acaccacct	780
477	gccctaccac	ctgcggagcc	cctgcccttc	aaatcccatc	acacggcctg	cgtaccaggg	840
479	cagcaacca	atcagtga	tttgggctat	ccacgcgctg	cggatcgtgg	ctaagtatct	900
481	gaagagggcc	gtcagaaatc	ccgatgatct	tgaagcaagg	tctcatatgc	acttggcaag	960
483	tgtttttgct	ggcatcggct	ttggaaatgc	tggtgttcac	ctgtgccatg	gaatgtctta	1020
485	cccaatttca	ggttttagtga	agatgtataa	agcaaaggat	tacaatgtgg	atcaccctact	1080
487	ggtgccccat	ggcctttctg	tggtgctcac	gtccccagcg	gtgttcactt	tcacggccca	1140
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493	ggatgttgat	gatggcctag	cagctgttgg	ttactccaaa	gctgatatcc	ccgcactagt	1320
495	gaaaggaacg	ctgccccagg	aaagggtcac	caagcttgca	ccctgtcccc	agtcagaaga	1380
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VERIFICATION SUMMARY

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L:20 M:270 C: Current Application Number differs, Replaced Current Application No

L:20 M:271 C: Current Filing Date differs, Replaced Current Filing Date